



RAW SEQUENCE LISTING

DATE: 07/10/2002

PATENT APPLICATION: US/09/679,664

TIME: 11:06:28

Input Set : A:\Pto.amc

Output Set: N:\CRF3\07102002\I679664.raw

4 <110> APPLICANT: NPS PHARMACEUTICALS, INC.
 5 STORMANN, Thomas
 7 <120> TITLE OF INVENTION: G-PROTEIN FUSION RECEPTORS AND CHIMERIC GABAB RECEPTORS
 9 <130> FILE REFERENCE: 072827-1801
 11 <140> CURRENT APPLICATION NUMBER: US 09/679,664
 12 <141> CURRENT FILING DATE: 2000-10-03
 14 <150> PRIOR APPLICATION NUMBER: US 60/080,671
 15 <151> PRIOR FILING DATE: 1998-04-03
 17 <150> PRIOR APPLICATION NUMBER: PCT/US99/07333
 18 <151> PRIOR FILING DATE: 1999-04-02
 20 <160> NUMBER OF SEQ ID NOS: 57
 22 <170> SOFTWARE: PatentIn version 3.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 612
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Human
 29 <220> FEATURE:
 30 <221> NAME/KEY: misc_feature
 31 <223> OTHER INFORMATION: CaR extracellular domain
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 37 1 5 10 15
 39 Thr Ser Ala Tyr Gly Pro Asp Gln Arg Ala Gln Lys Lys Gly Asp Ile
 40 20 25 30
 42 Ile Leu Gly Gly Leu Phe Pro Ile His Phe Gly Val Ala Ala Lys Asp
 43 35 40 45
 45 Gln Asp Leu Lys Ser Arg Pro Glu Ser Val Glu Cys Ile Arg Tyr Asn
 46 50 55 60
 48 Phe Arg Gly Phe Arg Trp Leu Gln Ala Met Ile Phe Ala Ile Glu Glu
 49 65 70 75 80
 51 Ile Asn Ser Ser Pro Ala Leu Leu Pro Asn Leu Thr Leu Gly Tyr Arg
 52 85 90 95
 54 Ile Phe Asp Thr Cys Asn Thr Val Ser Lys Ala Leu Glu Ala Thr Leu
 55 100 105 110
 57 Ser Phe Val Ala Gln Asn Lys Ile Asp Ser Leu Asn Leu Asp Glu Phe
 58 115 120 125
 60 Cys Asn Cys Ser Glu His Ile Pro Ser Thr Ile Ala Val Val Gly Ala
 61 130 135 140
 63 Thr Gly Ser Gly Val Ser Thr Ala Val Ala Asn Leu Leu Gly Leu Phe
 64 145 150 155 160
 66 Tyr Ile Pro Gln Val Ser Tyr Ala Ser Ser Ser Arg Leu Leu Ser Asn
 67 165 170 175
 69 Lys Asn Gln Phe Lys Ser Phe Leu Arg Thr Ile Pro Asn Asp Glu His

ENTERED

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70          180          185          190
72 Gln Ala Thr Ala Met Ala Asp Ile Ile Glu Tyr Phe Arg Trp Asn Trp
73          195          200          205
75 Val Gly Thr Ile Ala Ala Asp Asp Asp Tyr Gly Arg Pro Gly Ile Glu
76          210          215          220
78 Lys Phe Arg Glu Glu Ala Glu Glu Arg Asp Ile Cys Ile Asp Phe Ser
79 225          230          235          240
81 Glu Leu Ile Ser Gln Tyr Ser Asp Glu Glu Glu Ile Gln His Val Val
82          245          250          255
84 Glu Val Ile Gln Asn Ser Thr Ala Lys Val Ile Val Val Phe Ser Ser
85          260          265          270
87 Gly Pro Asp Leu Glu Pro Leu Ile Lys Glu Ile Val Arg Arg Asn Ile
88          275          280          285
90 Thr Gly Lys Ile Trp Leu Ala Ser Glu Ala Trp Ala Ser Ser Ser Leu
91          290          295          300
93 Ile Ala Met Pro Gln Tyr Phe His Val Val Gly Gly Thr Ile Gly Phe
94 305          310          315          320
96 Ala Leu Lys Ala Gly Gln Ile Pro Gly Phe Arg Glu Phe Leu Lys Lys
97          325          330          335
99 Val His Pro Arg Lys Ser Val His Asn Gly Phe Ala Lys Glu Phe Trp
100          340          345          350
102 Glu Glu Thr Phe Asn Cys His Leu Gln Glu Gly Ala Lys Gly Pro Leu
103          355          360          365
105 Pro Val Asp Thr Phe Leu Arg Gly His Glu Glu Ser Gly Asp Arg Phe
106          370          375          380
108 Ser Asn Ser Ser Thr Ala Phe Arg Pro Leu Cys Thr Gly Asp Glu Asn
109 385          390          395          400
111 Ile Ser Ser Val Glu Thr Pro Tyr Ile Asp Tyr Thr His Leu Arg Ile
112          405          410          415
114 Ser Tyr Asn Val Tyr Leu Ala Val Tyr Ser Ile Ala His Ala Leu Gln
115          420          425          430
117 Asp Ile Tyr Thr Cys Leu Pro Gly Arg Gly Leu Phe Thr Asn Gly Ser
118          435          440          445
120 Cys Ala Asp Ile Lys Lys Val Glu Ala Trp Gln Val Leu Lys His Leu
121          450          455          460
123 Arg His Leu Asn Phe Thr Asn Asn Met Gly Glu Gln Val Thr Phe Asp
124 465          470          475          480
126 Glu Cys Gly Asp Leu Val Gly Asn Tyr Ser Ile Ile Asn Trp His Leu
127          485          490          495
129 Ser Pro Glu Asp Gly Ser Ile Val Phe Lys Glu Val Gly Tyr Tyr Asn
130          500          505          510
132 Val Tyr Ala Lys Lys Gly Glu Arg Leu Phe Ile Asn Glu Glu Lys Ile
133          515          520          525
135 Leu Trp Ser Gly Phe Ser Arg Glu Val Pro Phe Ser Asn Cys Ser Arg
136          530          535          540
138 Asp Cys Leu Ala Gly Thr Arg Lys Gly Ile Ile Glu Gly Glu Pro Thr
139 545          550          555          560
141 Cys Cys Phe Glu Cys Val Glu Cys Pro Asp Gly Glu Tyr Ser Asp Glu
142          565          570          575

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144 Thr Asp Ala Ser Ala Cys Asn Lys Cys Pro Asp Asp Phe Trp Ser Asn
145          580                      585                      590
147 Glu Asn His Thr Ser Cys Ile Ala Lys Glu Ile Glu Phe Leu Ser Trp
148          595                      600                      605
150 Thr Glu Pro Phe
151      610
154 <210> SEQ ID NO: 2
155 <211> LENGTH: 590
156 <212> TYPE: PRT
157 <213> ORGANISM: Human
159 <220> FEATURE:
160 <221> NAME/KEY: misc_feature
161 <223> OTHER INFORMATION: GABA-betaR1a extracellular domain
163 <400> SEQUENCE: 2
166 Met Leu Leu Leu Leu Leu Ala Pro Leu Phe Leu Arg Pro Pro Gly
167 1          5          10          15
169 Ala Gly Gly Ala Gln Thr Pro Asn Ala Thr Ser Glu Gly Cys Gln Ile
170          20          25          30
172 Ile His Pro Pro Trp Glu Gly Gly Ile Arg Tyr Arg Gly Leu Thr Arg
173          35          40          45
175 Asp Gln Val Lys Ala Ile Asn Phe Leu Pro Val Asp Tyr Glu Ile Glu
176          50          55          60
178 Tyr Val Cys Arg Gly Glu Arg Glu Val Val Gly Pro Lys Val Arg Lys
179 65          70          75          80
181 Cys Leu Ala Asn Gly Ser Trp Thr Asp Met Asp Thr Pro Ser Arg Cys
182          85          90          95
184 Val Arg Ile Cys Ser Lys Ser Tyr Leu Thr Leu Glu Asn Gly Lys Val
185          100         105         110
187 Phe Leu Thr Gly Gly Asp Leu Pro Ala Leu Asp Gly Ala Arg Val Asp
188          115         120         125
190 Phe Arg Cys Asp Pro Asp Phe His Leu Val Gly Ser Ser Arg Ser Ile
191          130         135         140
193 Cys Ser Gln Gly Gln Trp Ser Thr Pro Lys Pro His Cys Gln Val Asn
194 145         150         155         160
196 Arg Thr Pro His Ser Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe
197          165         170         175
199 Pro Met Ser Gly Gly Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val
200          180         185         190
202 Glu Met Ala Leu Glu Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp
203          195         200         205
205 Tyr Glu Leu Lys Leu Ile His His Asp Ser Lys Cys Asp Pro Gly Gln
206          210         215         220
208 Ala Thr Lys Tyr Leu Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile
209 225         230         235         240
211 Ile Leu Met Pro Gly Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala
212          245         250         255
214 Ala Arg Met Trp Asn Leu Ile Val Leu Ser Tyr Gly Ser Ser Pro
215          260         265         270
217 Ala Leu Ser Asn Arg Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro

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218          275          280          285
220 Ser Ala Thr Leu His Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp
221          290          295          300
223 Gly Trp Lys Lys Ile Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr
224 305          310          315          320
226 Ser Thr Leu Asp Asp Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu
227          325          330          335
229 Ile Thr Phe Arg Gln Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys
230          340          345          350
232 Asn Leu Lys Arg Gln Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu
233          355          360          365
235 Thr Glu Ala Arg Lys Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe
236          370          375          380
238 Gly Lys Lys Tyr Val Trp Phe Leu Ile Gly Trp Ile Ala Asp Asn Trp
239 385          390          395          400
241 Phe Lys Ile Tyr Asp Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr
242          405          410          415
244 Glu Ala Val Glu Gly His Ile Thr Thr Glu Ile Val Met Leu Asn Pro
245          420          425          430
247 Ala Asn Thr Arg Ser Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu
248          435          440          445
250 Lys Leu Thr Lys Arg Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe
251          450          455          460
253 Gln Glu Ala Pro Leu Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala
254 465          470          475          480
256 Leu Asn Lys Thr Ser Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu
257          485          490          495
259 Asp Phe Asn Tyr Asn Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala
260          500          505          510
262 Met Asn Ser Ser Ser Phe Glu Gly Val Ser Gly His Val Val Phe Asp
263          515          520          525
265 Ala Ser Gly Ser Arg Met Ala Trp Thr Leu Ile Glu Gln Leu Gln Gly
266          530          535          540
268 Gly Ser Tyr Lys Lys Ile Gly Tyr Tyr Asp Ser Thr Lys Asp Asp Leu
269 545          550          555          560
271 Ser Trp Ser Lys Thr Asp Lys Trp Ile Gly Gly Ser Pro Pro Ala Asp
272          565          570          575
274 Gln Thr Leu Val Ile Lys Thr Phe Arg Phe Leu Ser Gln Lys
275          580          585          590
278 <210> SEQ ID NO: 3
279 <211> LENGTH: 473
280 <212> TYPE: PRT
281 <213> ORGANISM: Human
283 <220> FEATURE:
284 <221> NAME/KEY: misc_feature
285 <223> OTHER INFORMATION: GABA-betaR1b extracellular domain
287 <400> SEQUENCE: 3
290 Met Gly Pro Gly Ala Pro Phe Ala Arg Val Gly Trp Pro Leu Pro Leu
291 1          5          10          15

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293 Leu Val Val Met Ala Ala Gly Val Ala Pro Val Trp Ala Ser His Ser
294      20      25      30
296 Pro His Leu Pro Arg Pro His Ser Arg Val Pro Pro His Pro Ser Ser
297      35      40      45
299 Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly
300      50      55      60
302 Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu
303 65      70      75      80
305 Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu
306      85      90      95
308 Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu
309      100     105     110
311 Tyr Glu Leu Leu Asn Tyr Asp Pro Ile Lys Ile Ile Leu Met Pro Gly
312      115     120     125
314 Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn
315      130     135     140
317 Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg
318 145     150     155     160
320 Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His
321      165     170     175
323 Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile
324      180     185     190
326 Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp
327      195     200     205
329 Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln
330      210     215     220
332 Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln
333 225     230     235     240
335 Asp Ala Arg Ile Ile Val Gly Leu Phe Tyr Glu Thr Glu Ala Arg Lys
336      245     250     255
338 Val Phe Cys Glu Val Tyr Lys Glu Arg Leu Phe Gly Lys Lys Tyr Val
339      260     265     270
341 Trp Phe Leu Ile Gly Trp Tyr Ala Asp Asn Trp Phe Lys Ile Tyr Asp
342      275     280     285
344 Pro Ser Ile Asn Cys Thr Val Asp Glu Met Thr Glu Ala Val Glu Gly
345      290     295     300
347 His Ile Thr Thr Glu Ile Val Met Leu Asn Pro Ala Asn Thr Arg Ser
348 305     310     315     320
350 Ile Ser Asn Met Thr Ser Gln Glu Phe Val Glu Lys Leu Thr Lys Arg
351      325     330     335
353 Leu Lys Arg His Pro Glu Glu Thr Gly Gly Phe Gln Glu Ala Pro Leu
354      340     345     350
356 Ala Tyr Asp Ala Ile Trp Ala Leu Ala Leu Ala Leu Asn Lys Thr Ser
357      355     360     365
359 Gly Gly Gly Gly Arg Ser Gly Val Arg Leu Glu Asp Phe Asn Tyr Asn
360      370     375     380
362 Asn Gln Thr Ile Thr Asp Gln Ile Tyr Arg Ala Met Asn Ser Ser Ser
363 385     390     395     400
365 Phe Glu Gly Val Ser Gly His Val Val Phe Asp Ala Ser Gly Ser Arg

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/679,664

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Input Set : A:\Pto.amc
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; Xaa Pos. 13
Seq#:21; N Pos. 38
Seq#:40; N Pos. 3178,3179,3180,3181,3182,3183,3184,3185,3186,3187,3188,3189
Seq#:40; N Pos. 3190,3191,3192,3193,3194,3195,3196,3197,3198,3199,3200,3201
Seq#:40; N Pos. 3202,3203,3204,3205,3206,3207,3208,3209,3210,3211,3212,3213
Seq#:40; N Pos. 3214,3215,3216,3217,3218,3219,3220,3221,3222,3223,3224,3225
Seq#:40; N Pos. 3226,3227,3228,3229,3230,3231,3232,3233,3234,3235,3236,3237
Seq#:40; N Pos. 3238,3239,3240
Seq#:45; Xaa Pos. 464
Seq#:50; Xaa Pos. 379

VARIABLE LOCATION SUMMARY

DATE: 07/10/2002

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Use of n's or Xaa's(NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:4; Xaa Pos. 13

Seq#:21; N Pos. 38

Seq#:40; N Pos. 3178,3179,3180,3181,3182,3183,3184,3185,3186,3187,3188,3189

Seq#:40; N Pos. 3190,3191,3192,3193,3194,3195,3196,3197,3198,3199,3200,3201

Seq#:40; N Pos. 3202,3203,3204,3205,3206,3207,3208,3209,3210,3211,3212,3213

Seq#:40; N Pos. 3214,3215,3216,3217,3218,3219,3220,3221,3222,3223,3224,3225

Seq#:40; N Pos. 3226,3227,3228,3229,3230,3231,3232,3233,3234,3235,3236,3237

Seq#:40; N Pos. 3238,3239,3240

Seq#:45; Xaa Pos. 464

Seq#:50; Xaa Pos. 379

VERIFICATION SUMMARY

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Input Set : A:\Pto.amc

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L:397 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:397 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0
L:1679 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
L:4660 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:3120
L:4662 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:3180
L:5399 M:283 W: Missing Blank Line separator, <220> field identifier
L:5642 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:448
L:6805 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:368